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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-967-301-2.res made by bobryen on Wed 16 Jul :03 15:58:51-PDT.

Query sequence being compared:US-09-967-301-2 (1-238)
  File : US09967301.pep
Number of sequences searched: 3
Number of scores above cutoff: 3

----
    1. US-09-967-301-2 Sequence 2, Application US   238   238   238   1.73   0

The list of other best scores is:

                                                           Init. Opt.
Sequence Name   Description   Length Score Score Sig. Frame
----
    2. US-09-967-301-4 Sequence 4, Application US 238   237   237   0.00   0
    3. US-09-967-301-3 Sequence 3, Application US 238   237   237   0.00   0

1. US-09-967-301-2 (1-238)
   US-09-967-301-2 Sequence 2, Application US/09967301

Initial Score   =   238   Optimized Score =   238   Significance = 1.73
Residue Identity =   100%   Matches   =   238   Mismatches   =   0
Gaps   =   0   Conservative Substitutions =   0

```
X                    10        20        30        40        50        60        70
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFS
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFS
X                    10        20        30        40        50        60        70

                    80        90       100       110       120       130       140
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
                    80        90       100       110       120       130       140

                   150       160       170       180       190       200       210
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
                   150       160       170       180       190       200       210

                   220       230       X
HMVLLEFVTAAGITHGMDELYK
|||||||||||||||||||||
HMVLLEFVTAAGITHGMDELYK
                   220       230       X
```

2. US-09-967-301-4 Sequence 4, Application US/09967301
   US-09-967-301-4 Sequence 4, Application US/09967301

Initial Score   =   237   Optimized Score =   237   Significance = 0.00
Residue Identity =   98%   Matches   =   235   Mismatches   =   3
Gaps   =   0   Conservative Substitutions =   0

```
X                    10        20        30        40        50        60        70
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFSYGVQCFS
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLTYGVQCFS
X                    10        20        30        40        50        60        70

                    80        90       100       110       120       130       140
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
                    80        90       100       110       120       130       140

                   150       160       170       180       190       200       210
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
                   150       160       170       180       190       200       210

                   220       230       X
HMVLLEFVTAAGITHGMDELYK
|||||||||||||||||||||
HMVLLEFVTAAGITHGMDELYK
                   220       230       X
```

```
     100-
       |
   N  50-
   U  50-
   M  -
   B  -
   E  -
   R  -
       |
   O  -
   F  10-
       |
   S  5-
   E  -
   Q  -
   U  -
   E  -
   N  -
   C  -
   E  -
   S   0------------------------------------------------
       | | | | | | | | | | |
SCORE  0 26 53 79 106 132 159 185 212 238
STDEV                                          238
```

PARAMETERS

```
Similarity matrix          PAM-150    K-tuple                    1
Threshold level of sim.       16%
Mismatch penalty               1       Joining penalty          20
Gap penalty                 5.00       Window size             238
Gap size penalty            0.05
Cutoff score                   1
Randomization group            0
```

SEARCH STATISTICS

```
               Mean    Median   Standard Deviation
Scores:         237     238         0.58

Times:          CPU                 Total Elapsed
          00:00:00.00               00:00:00.00

Number of residues:        714
Number of sequences searched:        3
Number of scores above cutoff:       3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

                                        Init. Opt.
Sequence Name   Description   Length Score Score Sig. Frame

```
         220           230          X

3.  US-09-967-301-2 (1-238)
    US-09-967-301-3 Sequence 3, Application US/09967301

Initial Score    =    237  Optimized Score   =    237  Significance =  0.00
Residue Identity =    98%  Matches           =    235  Mismatches   =     3
Gaps             =     0   Conservative Substitutions  =          0

        10         20         30         40         50         60         70
X   MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGK_PVPWPTLVTTFSYGVQCFS
    |||||||||||||||:||||||||||||||||||||||||||||:||||||:||||||:|||||||||||||:|
    MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDAIYGKLTLKFICTGKLPVPWPTLVTTLSYGVQCFS
X       10         20         30         40         50         60         70

         80         90        100        110        120        130        140
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGCTLVNRIELKGIDFKEDGNILGHKLEYN
        80         90        100        110        120        130        140

        150        160        170        180        190        200        210
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
        150        160        170        180        190        200        210

        220        230        X
HMVLLEFVTAAGITHGMDELYK
|||||||||||||||||||||
HMVLLGFVTAAGITHGMDELYK
        220        230        X
```

```
> O <
OI IO   IntelliGenetics
> O <
```

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-967-301-3.res made by bobryen on Wed 16 Jul 103 15:59:33 PDT.

Query sequence being compared:US-09-967-301-3 (1-238)
Number of sequences searched: 3
Number of scores above cutoff: 3

Results of the initial comparison of US-09-967-301-3 (1-238) with:
       File : US09967301.pep

```
         N -
   100- U -
         U 50-
         M -
         B -
         E -
         R -
           -
         O -
         F 10-
           -
         S -
         E 5-
         Q -
         U -
         E -
         N -
         C -
         E -
         S 0 -----------------------------------------------------------------
SCORE 0    26    53    79   106   132   159   185   212   238
STDEV
```

PARAMETERS

```
Similarity matrix   PAM-150          K-tuple                 1
Threshold level of sim.   16%
Mismatch penalty    1                Joining penalty        20
Gap penalty         5.00             Window size           238
Gap size penalty    0.05
Cutoff score        1
Randomization group 0
```

SEARCH STATISTICS

```
              Mean    Median       Standard Deviation
Scores:       237      238              0.58

              CPU                  Total Elapsed
Times:     00:00:00.00            00:00:00.00

Number of residues:        714
Number of sequences searched:  3
Number of scores above cutoff: 3
```

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

```
                                              Init.   Opt.
Sequence Name   Description            Length  Score  Score  Sig.  Frame
```

---

1. US-09-967-301-3 Sequence 3, Application US   238   238   238   1.73   0

The list of other best scores is:

```
                                                     Init.  Opt.
Sequence Name   Description                   Length Score  Score  Sig. Frame
-------------   -----------                   ------ -----  -----  ---- -----
2. US-09-967-301-4 Sequence 4, Application US  238    237    237   0.00   0
3. US-09-967-301-2 Sequence 2, Application US  238    237    237   0.00   0
```

1. US-09-967-301-3 (1-238)
   US-09-967-301-3 Sequence 3, Application US/09967301

```
Initial Score      =   238     Optimized Score    =   238    Significance = 1.73
Residue Identity   =  100%     Matches            =   238    Mismatches   =  0
Gaps               =    0      Conservative Substitutions =    0
```

```
      X         10        20        30        40        50        60        70
              MSKGEELFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFS
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              MSKGEELFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFS
      X         10        20        30        40        50        60        70

                80        90       100       110       120       130       140
              RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
                80        90       100       110       120       130       140

               150       160       170       180       190       200       210
              YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
               150       160       170       180       190       200       210

               220       230       X
              HMVLLGFVTAAGITHGMDELYK
              |||||||||||||||||||||
              HMVLLGFVTAAGITHGMDELYK
               220       230       X
```

2. US-09-967-301-3 (1-238)
   US-09-967-301-4 Sequence 4, Application US/09967301

```
Initial Score      =   237     Optimized Score    =   237    Significance = 0.00
Residue Identity   =   99%     Matches            =   236    Mismatches   =  2
Gaps               =    0      Conservative Substitutions =    0
```

```
      X         10        20        30        40        50        60        70
              MSKGEELFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFS
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              MSKGEEFFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLIYGVQCFS
      X         10        20        30        40        50        60        70

                80        90       100       110       120       130       140
              RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
                80        90       100       110       120       130       140

               150       160       170       180       190       200       210
              YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
              YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
               150       160       170       180       190       200       210

               220       230       X
              HMVLLGFVTAAGITHGMDELYK
              |||||||||||||||||||||
              HMVLLEFVTAAGITHGMDELYK
               220       230       X
```

```
220        230        x



3. US-09-967-301-3 (1-238)
   US-09-967-301-2 Sequence 2, Application US/09967301

Initial Score    =  237   Optimized Score   =  237   Significance  =  0.00
Residue Identity =  98%   Matches           =  235   Mismatches    =     3
Gaps             =   0    Conservative Substitutions  =     0

X         10        20        30        40        50        60        70
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGK.PVPWPTLVTTLSYGVQCFS
||||||||||||||||||||||||||||||||||||||||||||||||:|:::|:|:::||||||||:|||||
MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGK.PVPWPTLVTTFSYGVCCFS
X         10        20        30        40        50        60        70

80        90        100       110       120       130       140
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYN
||||||||||:|||;:|||.:|||||||||||||||||||:::||;||;||:||||||||::||||.GHK.EYN
RYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHK.EYN
80        90        100       110       120       130       140

150       160       170       180       190       200       210
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGGVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRD
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||....
YNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKKD
150       160       170       180       190       200       210

220       230        x
HMVLLGFVTAAGITHGMDELYK
|||||:||||||||||||||||
HMVLLEFVTAAGITHGMDELYK
220       230        x
```